

EXHIBIT A

IN THE UNITED STATES DISTRICT COURT
IN AND FOR THE DISTRICT OF DELAWARE

NOVOZYMES A/S,
Plaintiff,
v
GENENCOR INTERNATIONAL, INC., and
ENZYME DEVELOPMENT CORPORATION,
Defendants.
NO. 05-160 (KAJ)

Wilmington, Delaware
Monday, March 6, 2006 at 9:00 a.m.
BENCH TRIAL

BEFORE: HONORABLE KENT A. JORDAN, U.S.D.C.J.

APPEARANCES:

YOUNG CONAWAY STARGATT & TAYLOR
BY: ROLIN P. BISSELL, ESQ., and
ANDREW A. LUNDREN, ESQ.

and

DARBY & DARBY, P.C.
BY: DAVID K. TELLEKSON, ESQ.,
KEVIN REINER, ESQ.,
ROBERT C. SULLIVAN, JR., ESQ.,
GEORGE HYKEL, ESQ.
SAMUEL S. WOODLEY, ESQ., and
ROERT SCHAFFER, ESQ.
(New York, New York)

Counsel for Plaintiff

Ellie Corbett Hannum
Registered Merit Reporter

Brian P. Gaffigan
Registered Merit Reporter

1 APPEARANCES: (Continued)

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3

MORRIS NICHOLS ARSHT & TUNNELL
BY: DONALD E. REID, ESQ.

4

and

5

6

JONES DAY
BY: THOMAS E. FRIEBEL, ESQ.
(New York, New York)

7

and

8

9

JONES DAY
BY: THARAN GREGORY LANIER, ESQ., and
JANE FROYD, ESQ.
(Menlo Park, California)

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and

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JONES DAY
BY: KENNETH R. ADAMO, ESQ.
(Dallas Texas)

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and

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GENENCOR INTERNATIONAL
BY: CHRISTOPHER STONE, ESQ.

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Counsel for Defendants

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Jorgensen - direct

1 MR. TELLEKSON: This is prepared by this witness
2 and it is a compilation of the steps of his process. I
3 could go through each and every step if I wanted. It would
4 take time. The witness is here to be cross-examined, so
5 it's not an out-of-court statement. The witness is here to
6 be cross-examined about his compilation of the steps of this
7 protocol.

8 THE COURT: Well, it clearly is an out-of-court
9 statement. So if you want to use this as an aid in having
10 him testify, go ahead. He hasn't moved it into evidence,
11 so the objection is premature. But if you want this
12 information in front of me, go ahead and put it in front of
13 me through your witness.

14 MR. TELLEKSON: Okay.

15 BY MR. TELLEKSON:

16 Q. Dr. Jorgensen, do you have an Exhibit 206 in front of
17 you?

18 A. Yes, on the screen. Yes.

19 Q. If you would like a hard copy it's also in front of
20 you in the hard copy, I believe.

21 A. Yes, I found it.

22 Q. And what is Exhibit 206?

23 A. That's the analysis we did on the G997 sample.

24 Q. And what is described in the 21 paragraphs of
25 Exhibit 206?

Jorgensen - direct

1 large amount, a small amount? How much would it be?

2 THE WITNESS: It would be --

3 THE COURT: Give me, like, if you can, stack of
4 paper? An estimate.

5 THE WITNESS: About 100 pages.

6 THE COURT: All of it together?

7 THE WITNESS: Yes.

8 THE COURT: Yes? All right. Your objection is
9 overruled. It's admitted. Let's go ahead.

10 MR. TELLEKSON: Thank you, Your Honor.

11 BY MR. TELLEKSON:

12 Q. And after following the protocol in Exhibit 206, were
13 you able to determine the sequence of G997?

14 A. Yes. In the sample, we found one met your amylase
15 component.

16 MR. TELLEKSON: Put up Exhibit 199, please.

17 BY MR. TELLEKSON:

18 Q. Dr. Jorgensen, can you tell us what is shown in
19 Exhibit 199?

20 A. That is the sequence of the alpha amylase that we
21 found in the G997 sample.

22 Q. And is this the sequence that you found by following
23 the protocol in Exhibit 206?

24 A. Yes, it is.

25 Q. Have you previously determined the sequence of

Jorgensen - redirect

1 Q. And whether or not there was more than one length of
2 a sequence there?

3 A. Yes, that's correct.

4 MR. TELLEKSON: Your Honor, I'd like to move
5 into evidence the exhibits that we discussed with
6 Dr. Jorgensen, 211, 212, 199 and 125. We already discussed
7 126.

8 THE COURT: 126. You mean --

9 MR. TELLEKSON: I'm sorry. 206. I'm sorry,
10 Your Honor.

11 THE COURT: Your position?

12 MR. LANIER: No objections, Your Honor.

13 THE COURT: They're admitted without objection.

14 * * * (Plaintiff's Exhibit Nos. 211, 212, 199 and 125
15 were received into evidence.)

16 THE COURT: I actually have a question that
17 might prompt something from you folks.

18 How long have you been with Novozymes, Doctor?

19 THE WITNESS: I've been there since 2001.

20 THE COURT: Are you familiar with the lab
21 protocols for handling samples?

22 THE WITNESS: We have a protocol for samples in
23 our lab but not in --

24 THE COURT: Then let's talk about your lab.

25 What is the protocol for handling a sample in your lab?

Arnold - direct

1 protein engineering.

2 The next step is to look at Spezyme Ethyl, which
3 is a product of protein engineering, and that is a modified
4 gene and a modified protein.

5 So this is the parent. It is an alpha amylase
6 and it is a bacillus stearothermophilus alpha amylase. That
7 is what this says here.

8 THE COURT: All right. Fine. Thanks.

9 Okay. We're at 12:30. Let me ask a couple
10 quick questions before we take this break. Just so that I
11 have a feel for what is in dispute. I know that at some
12 point, during the course of discovery, there was what the
13 plaintiff thought was an agreement about G997 and then that
14 turned out to be not an agreement about G997.

15 Why don't you remind me what that earlier
16 thinking by the plaintiff was and what the breakdown is real
17 quick, if you could.

18 MR. TELLEKSON: We thought it was not something
19 that really could be disputed, and we asked them to
20 stipulate.

21 THE COURT: What is this?

22 MR. TELLEKSON: I'm sorry. The sequence of G997
23 that you saw Dr. Jorgensen put up on the screen as
24 Exhibit 199. We thought that was the sequence and we asked
25 them to stipulate to that. We thought we had a stipulation

Arnold - direct

1 or we had an e-mail indicating they were going to agree to
2 it. And then time went past and suddenly it wasn't agreed
3 to and that's why we had to get some --

4 THE COURT: When was it that the understanding,
5 from your perspective, changed?

6 MR. TELLEKSON: You were involved in that. It
7 was maybe a month --

8 MR. SULLIVAN: Yes, I can address that, Your
9 Honor. It was about a week before the promise to give us a
10 supplementary interrogatory response. They agreed the
11 stipulation would be forthcoming and we had to remind them
12 several times to provide it. And then they finally provided
13 it. If you want to look at that interrogatory response you
14 will see it's the third response they've not been able to
15 confirm the actual sequence. And that's what happened.

16 THE COURT: All right.

17 MR. TELLEKSON: So then we produced
18 Dr. Jorgensen's results or some additional information to
19 back it up because we thought it was not going to be an
20 issue at trial.

21 THE COURT: Okay. And the specific documents in
22 that regard, that is, the e-mail exchanges, am I correct
23 those are in the court record at some point?

24 MR. SULLIVAN: Those were in some of the motions
25 in limine in the pretrial conference on that issue.

Arnold - direct

1 THE COURT: Right. I believe I have seen that.

2 All right. Is there anything that you folks
3 want to say in response to questions that I asked?

4 MR. LANIER: Very briefly, Your Honor. It's
5 important to distinguish between the two sequences of G997
6 we've been talking about. There has been no dispute about
7 the sequence of the protein encoded by the DNA. So that
8 the DNA sequence and the sequence of the protein as its
9 originally expressed. What they had asked us about was the
10 sequence of the protein as its sold as a final commercial
11 product. That was their request. That's the protein that
12 is floating out in the jugs and I have vials. What we told
13 them was we thought we could agree to that sequence.

14 We spent time with the client, and what we told
15 them was we could not confirm it for the reasons that we
16 spent some time talking with Dr. Jorgensen about. That is
17 the sequence as it's out in the world. We confirmed the
18 sequence as in the gene. The protein sequence as expressed
19 from the, or encoded by the DNA.

20 THE COURT: All right. Now, here is the problem
21 I'm having. On a foreshortened schedule to get to trial
22 that everybody wanted, I have a circumstance where it
23 appears that one side is giving the indication this isn't
24 going to be an issue at trial and then about a week before
25 the pretrial conference or so, if I have the timing right,

Arnold - direct

1 it is an issue. And then at trial, I'm getting questions
2 that at least indicate, and I don't know where you are going
3 with it, but at least indicate that I got a chain-of-custody
4 issue of a sort. Is this really, is it really G997?

5 Sounds like they're trying to put evidence on
6 responsive to that change in position, but I'm just putting
7 folks on notice that the timing here is going to make a
8 difference to me. And if that makes a difference in how
9 evidence is put on, I give you that information now. Okay?

10 MR. LANIER: May I make one comment on the
11 timing point, Your Honor --

12 THE COURT: Yes.

13 MR. LANIER: The request that they made came
14 about a week before, about two weeks before the end of
15 discovery. They said we needed you to confirm this or we'll
16 take a 30(b)(6) deposition. We said we can't. We did say
17 that. You will see that in the e-mail exchanges. It turns
18 out we couldn't. They didn't ask for the 30(b)(6)
19 deposition. They didn't ask for expedited discovery at the
20 pretrial conference. And so this is not a situation where
21 there has been an understanding for a long time. This is
22 also a claim that relates in great part to a claim added to
23 the case after the preliminary injunction hearing.

24 THE COURT: You know, I'm really reluctant to
25 have a case turn on something like this. I ought to be able

Arnold - direct

1 to decide whether this product that you are selling is or
2 isn't within the parameters of this claim. And I'm getting
3 a little uncomfortable where the maneuvering appears to be
4 headed which is, if I'm reading it right: Hey, Judge, you
5 can't say anything about whether we infringe or not because
6 we don't even know if what they are dealing with really is
7 our product. Maybe I'm reading too much into what is going
8 on here, but if I'm not reading too much, I'm going to order
9 the 30(b)(6) and I'm going to order it to take place
10 immediately. Like instantaneously, because I don't want to
11 have a close -- or I'll hold the evidence open, because I'm
12 not going to have this case turn on that. I'm just not.
13 It's not right. It's not appropriate to be deciding stuff
14 on what looks like it was discovery maneuvering. And I'm
15 not saying anybody is guilty or not guilty in how it turned
16 out.

17 I'm just saying that's an issue that we ought to
18 just put to bed. And if what it takes is a 30(b)(6), take
19 your 30(b)(6). You got tons of lawyers in this room, get a
20 representative, get a lawyer on each side and get in a room,
21 get something on the record. And then get me evidence so
22 we're done with this as an issue or at least as done with it
23 as we can be. It may be in the end that there is a failure
24 of proof. I'm not saying that that is not outside the realm
25 of possibility. It certainly is. It's certainly possible

Arnold - direct

1 that after all this is done there is a failure of proof.
2 But why we're talking about the constitution of the accused
3 product at this stage, it's a bit of a surprise. Let's
4 leave it at that.

5 MR. LANIER: Your Honor, the reason we are,
6 because the proteins in the world are uncertain.

7 THE COURT: Well, I want to emphasize I'm not
8 saying anything about infringement or noninfringement. I'm
9 just saying I would like to see what appears to me to be an
10 issue that can be resolved so I can make a decision on the
11 merits resolved. All right?

12 Okay. Let's take our hour. Okay?

13 (Lunch recess taken at 12:39 p.m.)

14 (Luncheon recess taken at 12:39, back in session
15 at session at 1:38 p.m.)

16 THE COURT: Good afternoon. Please be seated.
17 And let's continue with the examination of Dr. Arnold.

18 MR. TELLEKSON: Your Honor, before we start with
19 Dr. Arnold, I'm wondering if I could make a suggestion on
20 the issue we were talking about just before lunch.

21 THE COURT: Sure.

22 MR. TELLEKSON: We would think that this
23 shouldn't be in dispute and we would first ask that they
24 would stipulate to this.

25 THE COURT: They already said no to that so

Arnold - direct

1 let's move past it.

2 MR. TELLEKSON: The second thing is we expect to
3 provide some corroborating testimony through Dr. Arnold in
4 her testimony, but assuming there is still not willing to
5 stipulate at that point, what we would ask is that they
6 provide us a sample in a commercial jar labeled within
7 24 hours and -- of G997. And that we have two weeks to
8 analyze it so there is no doubt, no question that we had it
9 done exactly right.

10 MR. ADAMO: Deal.

11 THE COURT: All right. Done. Good.

12 MR. TELLEKSON: All right.

13 MR. ADAMO: We'll get working on it as soon as
14 we can, Your Honor.

15 THE COURT: All right. Thank you.

16 MR. ADAMO: You're welcome.

17 MR. TELLEKSON: And we might, we want to make
18 sure it was stored correctly and all that. We might need
19 a --

20 THE COURT: I'm confident that they'll stipulate
21 that their own sample is good; right?

22 MR. ADAMO: I won't put my thumb in it before I
23 give it to them, Your Honor. I promise.

24 Your Honor, believe me, I'm an officer of the
25 court. I will get them commercial product properly

Arnold - direct

1 maintained just as the client would have if he or she were
2 selling it to one of their customers.

3 THE COURT: Sounds like this is resolved.

4 MR. ADAMO: Thank you.

5 THE COURT: Thank you.

6 BY MR. TELLEKSON:

7 Q. Dr. Arnold --

8 MR. TELLEKSON: Let's put up Exhibit 126.

9 BY MR. TELLEKSON:

10 Q. I believe we were talking about the amino-acid
11 sequence of at least 95 percent homology to the parent and
12 here we have Exhibit 126 and the first issue is the
13 alignment.

14 Is that what you were testifying before lunch?

15 A. Please reorient me.

16 Q. All right. This is Exhibit, 126 which you heard
17 Dr. Devereux testify about.

18 How did you calculate the amino-acid sequence
19 with at least 95 percent homology to the parent?

20 A. That's right. Here is a comparison of the sequence
21 of G997 to Spezyme Ethyl, and the alignment is done. One
22 calculates then the percent identity. One calculates the
23 percent identity based on that alignment. Everything
24 except, everything in that sequence is identical, that's in
25 the amino acids that are aligned. And therefore, the

EXHIBIT B

ANALYSIS OF G997

A. SDS-PAGE Analysis

The protein components of the GZYME G997 sample were separated by SDS-PAGE as follows:

1. The sample was diluted twenty-fold with deionized water, followed by precipitation with trichloroacetic acid ("TCA"). The sample was resuspended in SDS-PAGE loading buffer containing 20 mM Tris-HCl pH 6.8, 2% SDS (w/v), 20% glycerol, 0.008% Bromophenol Blue ("BPB") (w/v), and 0.1 M dithiothreitol ("DTT"). The sample was incubated in this loading buffer for four minutes at 95 °C, and then loaded onto a standard, precast 4-20% SDS polyacrylamide gel for electrophoresis.
2. Following electrophoresis, the gel was incubated for five minutes in a standard blotting solution consisting of 10 mM 3-(cyclohexylamino)-1-propanesulfonic acid (CAPS) pH 11, and 6% methanol.
3. A ProBlott membrane from Applied Biosystems was used for electroblotting of the gel. The ProBlott membrane was soaked for one minute in pure methanol, and then placed in the blotting solution for five minutes. Electroblotting of the gel was carried out in a Semi Dry Blotter II apparatus from KemEnTec.
4. Following electroblotting, the ProBlott membrane was stained for 1 minute in 0.1% (w/v) Coomassie Brilliant Blue R-250 dissolved in a solution of 60% methanol, 1% acetic acid, and 39% distilled water. The ProBlott membrane was then incubated in 40% aqueous methanol for five minutes, followed by rinsing in deionized water. Finally, the ProBlott membrane was air dried.
5. Two protein bands of approximately equal intensity were identified on the ProBlott membrane that migrated at 55 kDa and 58 kDa. The proteins from each of these bands were recovered for further analysis.

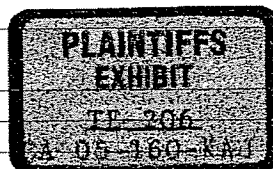
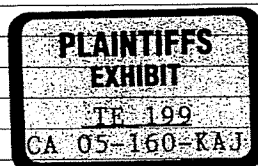


EXHIBIT C

Sequence of G997

AAPFNGTMMQ YFEWYLEDDG TLWTKVANE NNLSSLGITA LWLPPAYKGT SRSDVGYG VY
DLYDLGEFNQ KGTVRTKYGT KAQYLQAIQA AHAAGMQVYA DVVFDHKGGA DGETEWDAVE
VNPSDRNQEI SGTYQIQAWT KFDFPGRGNT YSSFKWRWYH EDGVDWDESR KLSRIYKFRG
IGKAWDWEVD TENGNYDYL M YADLMDHPE VVTELKNWGK WYVNTNIDG FRLDAVKHIK
FSFFPDWLSY VRSQTGKPLF TVGEYWSYDI NKLHNYITKT NGTMSLFDAP LHNKFYTASK
SGGAFDMRTL MTNTLMKDQP TLAVTFVDNH DTEPGQALQS WVDPEWKPLA YAFILTRQEG
YPCVFYGDYY GIPQYNIPSL KSKIDPELLIA RRDYAYGTQH DYLDHSDIIG WTREGVTEKP
GSGLAALITD GPGGSKWMYV GKQHAGKV FY DLTGNRSDTV TINS DGWGEF KVNGGSVSVW
VERKTT



CONFIDENTIAL

NV-200052

EXHIBIT D

NON-PUBLIC VERSION -- FILED UNDER SEAL
CONTAINS CONFIDENTIAL INFORMATION NOT FOR PUBLIC DISCLOSURE

EXHIBIT I:
PLAINTIFF'S MOTIONS *IN LIMINE* AND DEFENDANTS' RESPONSES THERETO

1. PLAINTIFF'S MOTION *IN LIMINE*
TO PRECLUDE DEFENDANTS FROM DISPUTING EVIDENCE
ON THE AMINO ACID SEQUENCE OF G997 PROFFERED BY NOVOZYMES

Throughout the entire discovery period, Plaintiff Novozymes A/S ("Novozymes") has repeatedly requested that the Defendants identify the amino acid sequence of the parent alpha-amylase from which Defendant Genencor International, Inc. ("Genencor") derived the variant alpha-amylase in its SPEZYME® ETHYL product. After SPEZYME® ETHYL's parent was identified as G@ZYME G997 ("G997"), Novozymes determined its amino acid sequence and repeatedly asked Genencor to confirm that the sequence was correct. Novozymes agreed to forego a 30(b)(6) deposition to confirm the sequence of G997 if Genencor would stipulate to the sequence as determined by Novozymes. Genencor expressly promised to provide the stipulation in the form of a supplemental interrogatory response. In the interrogatory response provided, however, Genencor did not confirm the sequence, but instead claimed that it was now unable to confirm or deny the sequence. Novozymes now moves pursuant to Rules 26-37 of the FED. R. Civ. P. to preclude Defendants from presenting evidence on the amino acid sequence of SPEZYME® ETHYL's parent.

Novozymes initiated this action for patent infringement of U.S. Patent No. 6,867,031 ("the '031 Patent") on March 15, 2005. The '031 Patent claims, *inter alia*, a variant alpha-amylase derived from a parent alpha-amylase.

In Interrogatory No. 5 of Plaintiff's First Set of Interrogatories, Novozymes requested that Genencor identify both the parent alpha-amylase from which SPEZYME® ETHYL was derived and the amino acid sequence of the parent alpha-amylase. Genencor identified the

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parent alpha-amylase as that obtained from *Bacillus stearothermophilus* strain ASP154, ATCC Deposit No. 39, 709, which Genencor dubs G@ZYME G997 or G997. Genencor, however, did not identify the amino acid sequence of G997. In a supplemental response to Novozymes' First Set of Interrogatories dated September 16, 2005, Genencor again failed to identify the amino acid sequence of G997.

Thereafter, Novozymes came to its own conclusion on the amino acid sequence of G997, and sought confirmation from Genencor of the accuracy of this sequence. Genencor promised to review the sequence and confirm the accuracy after such review. At one point, Genencor indicated its belief that the sequence was likely accurate, and promised to stipulate to the accuracy thereof. Genencor then provided a second supplemental response to Interrogatory No. 5, but again refused to confirm the accuracy of the G997 sequence provided by Novozymes. Instead, Genencor provided the sequence of the protein encoded by the G997 alpha-amylase gene.

Frustrated by Genencor's empty promises, Novozymes informed Genencor's counsel that absent confirmation of the G997 amino acid sequence, Novozymes would require a 30(b)(6) deposition on the issue. Genencor responded with the promise of confirmation through a third supplemental response to Interrogatory No. 5. Specifically, in an email from Jane Froyd (attorney for Defendants) to Robert C. Sullivan (attorney for Plaintiff) dated January 4, 2006, Ms. Froyd stated:

G997 Protein Sequence. We are discussing with the client today, but expect to confirm tomorrow, that the protein sequence of G997 as it is sold as a final, commercial product, is that set forth in Exhibit 11 of Dr. Arnold's First Report. We will formally confirm this in a supplemental interrogatory response. Please confirm that this eliminates the need for a 30(b)(6) deposition.

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In its third supplemental response to Interrogatory No. 5, however, Genencor stated that “based on a diligent investigation to date, Genencor is not able to confirm or deny” the sequence of G997 as determined by Novozymes.

In sum, Novozymes has repeatedly requested that Defendants identify the amino acid sequence of G997 by interrogatory request and follow up thereto. This information is directly relevant to Novozymes’ patent infringement claim. Rules 26 and 33 of the Fed. R. Civ. P. entitle Novozymes to a response to this interrogatory. Defendants have asserted no privilege in response to the interrogatory request. Defendants have directed Novozymes to NO documents that would provide an answer to this interrogatory request. Novozymes determined the amino acid sequence of G997 independently and sought confirmation of the accuracy from the Defendants. After a series of empty promises of confirmation, Defendants represented in a third supplementary response to the interrogatory that after a “diligent investigation” they cannot confirm or deny the accuracy of G997’s amino acid sequence as determined by Novozymes.

For the above stated reasons, Defendants should now be precluded from presenting evidence at trial on the amino acid sequence of G997.

EXHIBIT E

IN THE UNITED STATES DISTRICT COURT
FOR THE DISTRICT OF DELAWARE

NOVOZYMES A/S.

Plaintiff

C.A. No. 05-160-KAJ

GENENCOR INTERNATIONAL, INC., and
ENZYME DEVELOPMENT CORPORATION

Defendant

FOURTH DECLARATION OF CHRISTIAN ISAK JORGENSEN

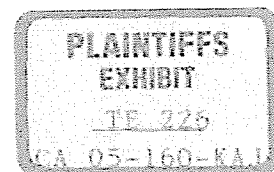
I, Christian Isak Jorgensen, do hereby declare as follows:

1 I am the same Christian Isak Jorgensen who submitted a Declaration signed on June 16, 2005 and in support of Novozymes' Motion for a Preliminary Injunction in the above-captioned law suit. I have also submitted Declarations signed on December 19, 2005, and January 31, 2006 for this same law suit. I hereby incorporate and affirm the statements in my prior Declarations in their entirety.

2 In my Declaration of December 19, 2005 (hereinafter referred to as my "Second Declaration") I described the analysis of what I understood to be a sample of an alpha-amylase product called GZYM1 G997. In that analysis, I found that the GZYM1 G997 sample contained a protein consisting of the sequence of amino acids 35-520 of the full length, pre-protein encoded by an alpha-amylase gene from the *Bacillus stearothermophilus* isolate ATCC 31,195.

3 The ATCC 31,195 alpha-amylase gene has been previously cloned, and is predicted to encode a sequence of 549 amino acids. This predicted amino acid sequence is available from the GenBank Database (Accession No. AAB86961).

A copy of the GenBank entry for ATCC 31,195 alpha-amylase (*ex* GenBank Accession No. AAB86961) was provided as Exhibit 1 of my Second Declaration.



4 I have now received a second sample of the GZYME G997 product for analysis. This second sample was provided by Genencor International, Inc., and has a Genencor product label identifying it as G-ZYME G997 Lot No. 107-04065-001. This second sample has been analyzed by me or by others working under my supervision and control, and compared to the G997 alpha-amylase sequence reported in my Second Declaration.

5 From my analysis, I have found that G-ZYME G997 Lot No. 107-04065-001 contains a protein that is identical to the G997 alpha-amylase protein described in my Second Declaration. More specifically, G-ZYME G997 Lot No. 107-04065-001 contains a protein consisting of the sequence of amino acids 38-520 of the predicted ATCC 31,195 alpha-amylase sequence. The complete amino acid sequence I have determined for the G-ZYME G997 Lot No. 107-04065-001 protein, which is identical to the G997 sequence reported in my Second Declaration, is attached hereto as Exhibit Tab 1.

6 The details of my analysis, and of the results obtained, are set forth *infra*, in this Fourth Declaration.

7 A. *SDS-PAGE Analysis of G997*

8 In a first analysis, the protein components of the second G997 sample (Lot No. 107-04065-001) were separated by SDS-PAGE following a protocol that is substantially identical to the SDS-PAGE protocol in my Second Declaration. Specifically, the sample was diluted 50- and 100-fold with deionized water. The sample was resuspended in SDS-PAGE loading buffer containing 20 mM Tris-HCl pH 6.8, 2% SDS (w/v), 20% glycerol, 0.008% Bromophenol Blue ("BPI") (w/v), and 0.1 M dithiothreitol ("DTT"). The sample was incubated in this loading buffer for four minutes at 95 °C, and then loaded onto a standard, precast 4-20% SDS polyacrylamide gel for electrophoresis.

9 Following electrophoresis, the gel was incubated for five minutes in a standard blotting solution consisting of 10 mM 3-(cyclohexylamino)-1-propanesulfonic acid (CAPS) pH 11, and 6% methanol. A ProBlott membrane from Applied Biosystems was used for electroblotting of the gel. The ProBlott membrane was soaked for one minute in pure methanol, and then placed in the blotting solution.

for five minutes. Electrobloeting of the gel was carried out in a Semi Dry Blotter II apparatus from KemEltec.

9 Following electroblotting, the ProBlott membrane was stained for 1 minute in 0.1% (w/v) Coomassie Brilliant Blue R-250 dissolved in a solution of 60% methanol, 1% acetic acid, and 39% distilled water. The ProBlott membrane was then incubated in 40% aqueous methanol for five minutes, followed by rinsing in deionized water. Finally, the ProBlott membrane was air dried.

10 Two protein bands of approximately equal intensity were identified on the ProBlott membrane that migrated at 55 kDa and 58 kDa. The proteins from each of these bands were recovered for further analysis.

B. N-Terminal Sequencing of the G997 Protein

11 The amino acid sequences of the proteins recovered by SDS-PAGE were analyzed by N-terminal sequencing. The 55 and 58 kDa bands were each cut out of the ProBlott membrane, and placed in the blotting cartridge of a Precise Protein Sequencer from Applied Biosystems.

12 N-terminal sequencing of the protein in these bands was carried out following the manufacturer's instructions, and as described in my previous Declaration. Briefly, the N-terminal amino acid sequence was determined from resulting chromatograms by comparing the retention time of the peaks in the chromatograms to retention times of PTH-amino-acids in a standard chromatogram. In addition, amino acid yields were determined by comparing the peak area to the corresponding standard peak area.

13 The protein recovered from the 58 kDa band was thus found to have the following N-terminal amino acid sequence: ADTKKLITSWG. The second protein, which was recovered from the 55 kDa band, was found to have the N-terminal amino acid sequence AAPFNGTMMQYF. This second

These N-terminal sequences are identical to those of the 58 and 55 kDa bands recovered from the previous sample of G-ZYME G997. See, ¶ 12 of my Second Declaration.

sequence is identical to the sequence of amino acid residues 35-46 of the ATCC 31,195 alpha-amylase sequence available from GenBank.

C. Molecular Weight Analysis of the G997 Protein

14. I have calculated the molecular weight of a protein having the amino acid sequence of the predicted ATCC 31,195 alpha-amylase at after the secretion signal on its N-terminus has been removed. That is to say, I have calculated the molecular weight of a protein having the sequence of residues 35-549 in the ATCC 31,195 alpha-amylase sequence from GenBank (Accession No. AAB86961). The average molecular weight of this protein, calculated using the program GPMW version 6.2 from Lighthouse Data, is 58,748.80 Da.

15. I, or others working under my supervision and control, have also analyzed the GZYMF G997 (Lot No. 107-04065-001) protein by mass spectroscopy ("MS"), and thereby measured its average molecular weight.

16. Specifically, 9 ml aliquots from the G997 sample were dialyzed overnight at 5 °C and against 20 liters of buffer containing a 5 mM Tris-HCl pH 9.5 and 2 mM CaCl₂. The dialyzed sample was filtered through a 0.45 µm filter to remove any precipitated material that may have been present, and was then applied to a Q-Sepharose FF column (26 x 120 mm) from Amersham Biosciences that had been equilibrated in 5 mM Tris-HCl pH 9.5 ("buffer A"). After application of protein sample, the column was washed with 10 column volumes of buffer A to remove unbound protein. Bound protein was eluted off of the column using a gradient of zero to 1 M NaCl in buffer A over 10 column volumes. Protein containing fractions were identified by their high absorbance of UV-light at 280 nm (A_{280}) as they eluted off the column. Fractions with a high A_{280} value were analyzed by SDS-PAGE to confirm that they contained the 55 kDa protein component. Fractions containing that protein were then combined and desalted by reverse-phase chromatography with a C4-reverse phase column from Millipore.

17. The resulting sample of purified protein was analyzed using an online MicroTOF FOCUS ESI mass spectrometer from Bruker Daltonics Inc. for exact mass measurements. A number of

mass peaks were observed at around 55992 Da. These peaks, which ranged from 55,667.3 Da to 56,477.6 Da, were separated by a spacing of 162 Da. These peaks are consistent with a protein that has been glycosylated with one or more hexose molecules.⁷

18 I have also calculated the molecular weight of the protein having the amino acid sequence of residues 35-520 of the ATCC 31,195 alpha-amylase protein sequence from GenBank (Accession No. AAB80961). I found that this protein has a calculated molecular weight of 55,342.85 Da. I have also calculated the molecular weight of the same protein that has been glycosylated with two hexose molecules, and found that the glycosylated protein has a calculated molecular weight of 55,667.15 Da. This calculated molecular weight is in accord with the measured molecular weight of the lowest glycosylated form of the protein observed at 55,667.3 Da.

D. Digestion of the G997 Protein

19 The protein component purified from GZYME G997 was further analyzed by digestion with cyanogen bromide (CNBr), in order to verify its determined amino acid sequence. CNBr cleaves peptide bonds specifically at the carboxylic site of methionine residues. Hence, by treating a protein with CNBr under suitable conditions, the protein can be broken down or "digested" into smaller peptide fragments that end in methionine ("M").

20 Treatment of a protein having the amino acid sequence at of the predicted ATCC 31,195 alpha-amylase from GenBank (Accession No. AAB80961) will produce a peptide fragment with a calculated monoisotopic molecular weight of 8,060.47 Da and having the amino acid sequence YVGRQHACKVFYDLTGNRSDTVTNSDQWGEFKVNGGSVSVWVPRKTTVSTIARPITTRPWTGLFVRWTEPRLVAWP.

However, if the protein's C-terminus ends at amino acid 520 of the ATCC 31,195 alpha-amylase sequence from GenBank, then this fragment will not be present. Instead, CNBr digestion of the protein

⁷ The molecular weight of a single hexose molecule is 162.14 Da, the spacing between the observed mass peaks.

will produce a peptide fragment with a calculated monoisotopic molecular weight of 5,256.64 Da, and having the amino acid sequence

YVGRQHAGKVFYDLTGNRSDTVTINSIDGWGEFKVNGGSVSVWVPRKTT

21. Purified protein from the GZYME G997 protein sample was buffer exchanged to 0.1 M HCl by a Microcon YM-10 filter device from Millipore. One crystal of CNBr was added to the sample, and the sample was incubated for four hours at 37 °C. A 0.5 µl aliquot from the digested protein sample was spotted directly to a MALDI-TOF target plate, to which 0.5 µl of CHCA matrix was then added, mixed, and allowed to dry. MALDI-TOF analysis of the sample was done using a Voyager DE-PRO workstation from Applied Biosystems for exact mass measurements.

22. No protein fragments were identified that had a molecular weight of 8,660.47 Da. However, a protein fragment was detected that had a measured monoisotopic molecular weight of 5,256.7 Da. Another protein fragment was observed that had a molecular weight of 5,419.3 Da. This second fragment is consistent with glycation of the 5,256.7 Da fragment by one hexose molecule.

23. The 5,256.7 and 5,419.3 Da protein fragments separated by MALDI-TOF were collected, and the sequence of their first twelve amino acid residues was determined by N-terminal sequencing. Specifically, BioBrene Plus pretreated filters were prepared for N-terminal sequencing by adding 15 µl of BioBrene Plus solution (Applied Biosystems) to the filter, and cleaned by running four cycles of the Filter Pre-cycle programme on a Procise Protein Sequencer (also from Applied Biosystems). The collected peptide fragments were then sequenced by adding 15 µl of the collected sample to the pretreated BioBrene Plus filter. The filter was then loaded onto the Protein Sequencer and sequenced using the Pulsed liquid method.

24. From this analysis, the sequence of the first twelve amino acid residues in the 5,256.7 and 5,419.3 Da fragments was determined to be YVGRQHAGKVFY. This sequence confirms that the C-terminal digestion fragment had been isolated.

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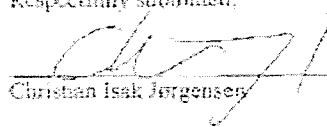
001

25. The results from this analysis confirm that GZYME G997 contains a protein having the amino acid sequence set forth at Exhibit 1 of this Fourth Declaration. This sequence is identical to the sequence of residues 35-520 of the ATCC 31,195 alpha-amylase sequence from GenBank (Accession No. AAB86961).

26. I declare under penalty of perjury pursuant to the laws of the United States of America that the foregoing statements are true and correct.

Respectfully submitted,

Dated: March 24, 2006


Christian Isak Jorgensen

Attachment:

Exhibit 1: G ZYME G997 (Lot No. 107-04065-001) amino acid sequence.

Sequence of G-ZYME G997
(Lot No. 107-04065-001)

1	AAEPNFTMGL YFEWYLEPDC ILWISVANEA NULSELGITA ENLPBAYKST	70
51	SRSTVQYGVY DLYDLGEFNG KOTVVKRYET KAGYLALIA AHAAGHVVYA	100
101	DVYFDHNGGA DGTENYDAVE VHPENALJEI SETYUIGAWT KSEPPGRCNT	130
151	YSSFKWRWYH EHGVDWIEHF KLERIKYHNS ICRADWWEVL TENGNVLYLK	160
201	YADLDWDHFF WTELEKWKLF WYVNTTNIHG EALLAVKHIE ESEFPIMLSY	230
251	VRS.TGRILF TVHEYMWYDE KHLINXITET KSTMLASDAI LHNKPYTASF	300
301	QMAEJHREL WNTENKILF PLAVTEVNNH STEPSALIS WYDHTFPIA	330
351	YAPILTRJES YPOVYGDY SIPTENTEDL KPLHILLIA HROVAVSTW	400
401	ELILRLGIF WTRF-VTNSP SEFLAALIE GYGLSRWAY. LK,SHAGWY	430
451	ELTHKSDTV TINSIGNGSE KXNGGVCOW VPRATY	460

EXHIBIT F

Woodley, Samuel

From: Greg Lanier [tglanier@JonesDay.com]
Sent: Friday, March 31, 2006 10:03 AM
To: Woodley, Samuel
Cc: dreid@mnat.com; Jane L Froyd; kradamo@jonesday.com
Subject: RE: G997 sample

Sam, Genencor will not stipulate to admissibility of the 4th Jorgenson Declaration, but it will stipulate that the amino acid sequence listed at exhibit 1 to that declaration is an amino acid sequence obtained by Novozymes by analysis of the sample of G-ZYME G997 provided by Genencor, that analysis being performed in a manner consistent with the analysis described in TE 206 (without waiver of defendants' objections (overruled) to that exhibit).

Greg

Tharan Gregory Lanier
Jones Day
2882 Sand Hill Road, Suite 240
Menlo Park, CA 94025
650-739-3941 (Direct)
650-739-3900 (Fax)
tglanier@jonesday.com

"Woodley, Samuel"
<swoodley@Darbyla
w.com>

03/31/2006 06:55
AM

"Greg Lanier"
<tglanier@JonesDay.com>

<dreid@mnat.com>, "Jane L Froyd"
<jfroyd@JonesDay.com>,
<kradamo@jonesday.com>

To

cc

Subject

RE: G997 sample

Dear Greg,

We have not heard from you on this since Tuesday. If we don't have your agreement to stipulate to the admissibility of the Jorgensen declaration by 3 pm Eastern time today, we will seek guidance from the Court.

Samuel S. Woodley, Ph.D.
Darby & Darby P.C.
805 Third Avenue
New York, New York 10022

(212) 527-7610 | direct
(212) 527-7701 | fax

<http://www.darbylaw.com>

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>-----Original Message-----

>From: Greg Lanier [mailto:tglanier@JonesDay.com]

>Sent: Tuesday, March 28, 2006 12:32 PM

>To: Woodley, Samuel

>Cc: dreid@mnat.com; Jane L Froyd; kradamo@jonesday.com

>Subject: RE: G997 sample

>

>

>Sam, we thought we were responding to the following request:

>

> we now ask that you let us know

>>whether Genencor is willing to stipulate that TE-123 is the

>amino acid

>>sequence of Genencor's GZYME-G997 alpha-amylase.

>

>In any event, we will review the new proposed stipulations and will respond.

>

>Greg

>

>Tharan Gregory Lanier

>Jones Day

>2882 Sand Hill Road, Suite 240

>Menlo Park, CA 94025

>650-739-3941 (Direct)

>650-739-3900 (Fax)

>tglanier@jonesday.com

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>

>

> "Woodley, Samuel"

>

> <swoodley@Darbyla

>

> w.com>

> To

>

"Greg Lanier"

>

<tglanier@JonesDay.com>

>

> 03/28/2006 09:25

> cc

>

AM

"Jane L Froyd"

>

<jfroyd@JonesDay.com>,

>

<kradamo@jonesday.com>,

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<dreid@mnat.com>

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>

Subject

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RE: G997 sample

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>Dear Greg:
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>You seem to have misunderstood the scope of our request. To
>clarify: Is Genencor willing to stipulate to the admissibility of Dr.
>Jorgensen's fourth Declaration as part of the trial record? Also, is
>Genencor willing to stipulate that the sequence at Exhibit 1 of that
>Declaration is the alpha amylase amino acid sequence he obtained by
>analyzing the commercial G997 sample provided by Genencor, following
>the procedure described in the Declaration?
>
>Please let us have your response by tomorrow.
>
>Samuel S. Woodley, Ph.D.
>Darby & Darby P.C.
>805 Third Avenue
>New York, New York 10022
>
>(212) 527-7610 | direct
>(212) 527-7701 | fax
>
><http://www.darbylaw.com>
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>212.527.7700 or 206.262.8900; and delete this email message and any
>attachments. Thank you for your assistance.
>
>
>>-----Original Message-----
>>From: Greg Lanier [mailto:tglanier@JonesDay.com]
>>Sent: Monday, March 27, 2006 5:46 PM
>>To: Woodley, Samuel
>>Cc: Jane L Froyd; kradamo@jonesday.com; dreid@mnat.com
>>Subject: Re: G997 sample
>>
>>
>>Sam, Genencor does not agree to stipulate that the sequence set forth
>>in TE 123 is "the" amino acid sequence of G-ZYME G997; that
>>there is a
>>single, reliably determinable amino acid sequence for G-ZYME G997; or
>>that the sequence(s), even if reliably determinable, is(are)
>>relevant.
>>As discussed at trial (see, eg., Tr. 156:20-157:2), Genencor will
>>stipulate that the sample delivered to Novozymes was a sample
>>of G-ZYME
>>G997 of the same type, maintained and delivered in the same manner,
>>and with the same accompanying materials, as if the sample were being

>You seem to have misunderstood the scope of our request. To
>clarify: Is Genencor willing to stipulate to the admissibility of Dr.
>Jorgensen's fourth Declaration as part of the trial record? Also, is
>Genencor willing to stipulate that the sequence at Exhibit 1 of that
>Declaration is the alpha amylase amino acid sequence he obtained by
>analyzing the commercial G997 sample provided by Genencor, following
>the procedure described in the Declaration?

```
>Samuel S. Woodley, Ph.D.  
>Darby & Darby P.C.  
>805 Third Avenue  
>New York, New York 10022
```

><http://www.darbylaw.com>

>>-----Original Message-----

>>Sam, Genencor does not agree to stipulate that the sequence set forth
>>in TE 123 is "the" amino acid sequence of G-ZYME G997; that
>there is a
>>single, reliably determinable amino acid sequence for G-ZYME G997; or
>>that the sequence(s), even if reliably determinable, is(are)
>relevant.
>>As discussed at trial (see, eg., Tr. 156:20-157:2), Genencor will
>>stipulate that the sample delivered to Novozymes was a sample
>of G-ZYME
>>G997 of the same type, maintained and delivered in the same manner,
>>and with the same accompanying materials, as if the sample were being

>>provided to a Genencor customer.

>>

>>Greg

>>

>>Tharan Gregory Lanier

>>Jones Day

>>2882 Sand Hill Road, Suite 240

>>Menlo Park, CA 94025

>>650-739-3941 (Direct)

>>650-739-3900 (Fax)

>>tglanier@jonesday.com

>>

>>

>>

>>

>>

>> "Woodley, Samuel"

>>

>> <swoodley@Darbyla

>>

>> w.com>

>> To

>>

"Greg Lanier"

>>

>><tglanier@JonesDay.com>, "Jane L

>> 03/24/2006 09:54

Froyd"

>><jfroyd@JonesDay.com>

>> AM

>>

cc

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>> Subject

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G997 sample

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>>Dear Greg:

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>>Novozymes' Christian Jorgensen has now characterized the G997

>>alpha-amylase sample from Genencor. Attached is a Fourth Declaration

>>from Dr. Jorgensen, describing that characterization and

>>setting forth,

>>in Exhibit 1, the G997 amino acid sequence. As you can see, Dr.

>>Jorgensen has found that this sample has the same amino acid sequence

>>that he had previously determined for G997 -- i.e., the amino acid

>>sequence at TE-123.

>>

>>In view of these results, we now ask that you let us know whether

>>Genencor is willing to stipulate that TE-123 is the amino

>acid sequence

>>of Genencor's GZYME-G997 alpha-amylase. Please let us have
>your answer
>>before close of business in New York next Monday, March 27, 2006. We
>>will then notify the court of the stipulation, so that the record can
>>be closed on this matter.
>>
>>Samuel S. Woodley, Ph.D.
>>Darby & Darby P.C.
>>805 Third Avenue
>>New York, New York 10022
>>
>>(212) 527-7610 | direct
>>(212) 527-7701 | fax
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